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Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Books

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Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

GenBank

Send

all to file

Range: from begin to end

☐ Reverse complemented strandFeatures: ☐ SNP ☐ CDD☒ MGC☐ 1: XM_211174. Reports PREDICTED: Homo s...[gi:27483466]

Links

LOCUS XM_211174 1021 bp mRNA linear PRI 20-AUG-2004

DEFINITION PREDICTED: Homo sapiens hypothetical LOC283710 (LOC283710), mRNA.

ACCESSION XM_211174

VERSION XM_211174.1 GI:27483466

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence (NT_010194) using gene prediction method: GNOMON, supported by EST evidence.

Also see:

[Documentation of NCBI's Annotation Process](#)

FEATURES

Location/Qualifiers

source 1..1021
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="15"

gene 1..1021
/gene="LOC283710"
/note="Derived by automated computational analysis using gene prediction method: GNOMON."
/db_xref="GeneID:283710"
/db_xref="InterimID:283710"

CDS 106..510
/gene="LOC283710"
/codon_start=1
/product="hypothetical protein XP_211174"
/protein_id="XP_211174.1"
/db_xref="GI:27483467"
/db_xref="GeneID:283710"
/db_xref="InterimID:283710"
/translation="MGVFTMQGGIPCCSTIRFGTTPPPRPHQRASAMPRRGPOQTRQ
DPPVGP KAGGRAAPPNSQDACSTPHAPLSASGEHPATPRHHPGYIPPSHAWSGALEM
SEIQAFP KESGLEGLPPFAELHMTTADDRPH"

ORIGIN

```

1  aaggatgagc aggtctctg ccatctgcc accaactttt caagttactt ttacccacct
61  tcaaaattac atctgctttt agcaagaatt actgatgtga taaagatggg agtggtcacc
121 atgcaagggc aggggatccc ctgctgctcc accatcagat ttgggacacc accccccccc
181 cggccccacc agagggcatc agctatgcct agaaggggac cacaacagac tcgacaggat
241 ccaccggttg ggcccaaggc aggaggaagg gcggcgcccc caaactccca ggacgcctgc
301 agcacccccc acgcgcgctt ctccgcctct ggggagcatc ctgccacccc ccgacacaca
361 caccgccggt acatcccgcc ttctcacgct tggtcaggcg ctctggagat gtcggagatc
421 caggcttttc ctaaagagtc aggattgga ggcggactcc caccgtttgc tgagctccac
481 atgacaacag cagacgacag gccgcactga tccacactgg cttacagggtg ctgtcacaca

```

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661 accattgttt acatgtcggt caggactgct gactaaacac tttcaagcac agtggaccct
721 tgaacaacgc aggttcaaac tgtgcaggtc caccacagg gatgtttttc aatcagagtt
781 ataccaagtg tccctgcctc tcctgcctcc cttcccactt cctccatgtc ttcctctctg
841 ccaccctgag gcagcaagac cagcccctcc tcctcagcca ctcaacatga agacaacgag
901 gatgaagact tctatgataa tccacttcca cttagtaaat gctttctctt atgatattct
961 taatgacatt ttattttccc aagcttagtt tattgtaaga atacagtata aatacacata
1021 c
```

//

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Dec 16 2004 18:01:17



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Find (Accessions, GI numbers or Fasta style SeqIds) XM_211174

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Gi	Version	Update Date
27483466	1	Aug 20 2004 9:44 AM
27483466	1	Apr 28 2003 1:46 PM

Entrez

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Query= gi|27483466|ref|XM_211174.1| PREDICTED: Homo sapiens hypothetical LOC283710 (LOC283710), mRNA (1021 letters)

Help/FAQ

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

Check sequence revision history

How to create WWW links to Entrez

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Cubby

Related resources

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Reference sequence project

LocusLink

Query: 1 aaggatgagcaggctctctgccatctgccacaaacttttcaagttactttaccacct 60

|||||

Sbjct: 1 aaggatgagcaggctctctgccatctgccacaaacttttcaagttactttaccacct 60

Query: 61 tcaaaattacatctgcttttagcaagaattactgatgtgataaagatgggagtggtcacc 120

|||||

Sbjct: 61 tcaaaattacatctgcttttagcaagaattactgatgtgataaagatgggagtggtcacc 120

Query: 121 atgcaagggcaggggatcccctgctgctccaccatcagatttgggacaccannnnnnnn 180

|||||

Sbjct: 121 atgcaagggcaggggatcccctgctgctccaccatcagatttgggacaccaccccccccc 180

Query: 181 ngccccaccagagggcacatgcctatgcctagaaggggaccacacagactcgacaggat 240

|||||

Sbjct: 181 cggccccaccagagggcacatgcctatgcctagaaggggaccacacagactcgacaggat 240

Clusters of orthologous groups

Protein reviews on the web

Query: 241 ccaccggttgggcccaaggcaggaggaaggcgggcgcccccaactcccaggacgcctgc 300
|||||
Sbjct: 241 ccaccggttgggcccaaggcaggaggaaggcgggcgcccccaactcccaggacgcctgc 300

Query: 301 agcacccccacgcgcgcctctccgcctctgaggagcatcctgccaccccccgacacaca 360
|||||
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|||||
Sbjct: 361 caccgcggtacatccccgccttctcacgccttggtcaggcgctctggagatgtcggagatc 420

Query: 421 caggcttttctctaaagatcaggattggaaggcggactcccaccggttgctgagctccac 480
|||||
Sbjct: 421 caggcttttctctaaagatcaggattggaaggcggactcccaccggttgctgagctccac 480

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|||||
Sbjct: 481 atgacaaacagcagacagcaggccgcactgatcccacctgggttacagggtgctgtcacaca 540

Query: 541 ggtacgccttcttgatcatcagtcaccatttgccccctgcgagcaaccctgtcttggga 600
|||||
Sbjct: 541 ggtacgccttcttgatcatcagtcaccatttgccccctgcgagcaaccctgtcttggga 600

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|||||
Sbjct: 601 ggaaggtccttgccgacacccgcctctccccacccttaggtcccttgctccttcattca 660

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Sbjct: 661 accattgtttacatgtcgttcaggactgctgactaaacactttcaagcacagtggaacct 720

Query: 721 tgaacaacgcaggttcaaaactgtgcaggtccaccacagggatgtttttcaatcagagtt 780
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Sbjct: 781 ataccaagtgtccctgcctctcctgcctccctccacttcccatgtcttccctctctg 840

Query: 841 ccacctgagggcagcaagaccagccctcctcctcagccactcaacatgaagacaacgag 900
|||||
Sbjct: 841 ccacctgagggcagcaagaccagccctcctcctcagccactcaacatgaagacaacgag 900

Query: 901 gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatatct 960
|||||
Sbjct: 901 gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatatct 960

Query: 961 taatgacattttattttcccaagcttagttattgtgaagaatacagtatataaacacata 1020
|||||
Sbjct: 961 taatgacattttattttcccaagcttagttattgtgaagaatacagtatataaacacata 1020

Query: 1021 c 1021

|

Sbjct: 1021 c 1021

Score = 32.2 bits (16), Expect = 2e-04
Identities = 16/16 (100%)
Strand = Plus / Minus

Query: 129 gcaggggatccccctgc 144
|||||
Sbjct: 144 gcaggggatccccctgc 129

Lambda K H

1.37 0.711 1.31

Gapped

Lambda K H

1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 3
length of query: 1021
length of database: 1021
effective HSP length: 9
effective length of query: 1012
effective length of database: 1012
effective search space: 1024144
effective search space used: 1024144

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 9 (18.3 bits)

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Genome

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PMC

Taxonomy

OMIM

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Find (Accessions, GI numbers or Fasta style SeqIds)

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Show

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Gi Version

Update Date

27483466

1

Aug 20 2004 9:44 AM

27483466

1

Apr 28 2003 1:46 PM

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Accession = XM_211174, Locus = XM_211174

=====

Help/FAQ

Differences in LOCUS names:

old: "LOCUS XM_211174
28-APR-2003"

1021 bp mRNA linear PRI

new: "LOCUS XM_211174
20-AUG-2004"

1021 bp mRNA linear PRI

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

Check sequence revision history

Differences in DEFINITION:

old: "Homo sapiens LOC283710 (LOC283710), mRNA."

How to create WWW links to Entrez

new: "PREDICTED: Homo sapiens hypothetical LOC283710 (LOC283710), mRNA."

LinkOut

Differences in REFERENCE:

Old reference:

refline: "1 (bases 1 to 1021)"

authors: "International Human Genome Sequencing Consortium."

title: "The DNA sequence of Homo sapiens"

journal: "Unpublished (2003)"

"1 (bases 1 to 1021)"
"International Human Genome Sequencing Consortium."
"The DNA sequence of Homo sapiens"
"Unpublished (2003)"

Related resources

BLAST

Reference sequence project

Differences in COMMENT:

LocusLink

old: "MODEL REFSEQ: This record is predicted by automated computational

Clusters of orthologous groups

analysis. This record is derived from an annotated genomic sequence (NT_010194) using gene prediction method: BLAST, supported by EST

Protein reviews on the web

evidence. Also see: Documentation of NCBI's Annotation Process "new: "MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence (NT_010194) using gene prediction method: GNOMON, supported by EST

evidence. Also see: Documentation of NCBI's Annotation Process "

Differences in FEATURE.CDS:

 Changed feature CDS 106..510
 New /db_xref = "GeneID:283710"

Differences in FEATURE.gene:

 Changed feature gene 1..1021
 New /db_xref = "GeneID:283710"
 New /note = "Derived by automated computational
 analysis using gene prediction method:
 GNOMON."

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